

Supporting information for Ferro *et al.* (2002) *Proc. Natl. Acad. Sci. USA*,
10.1073/pnas.172390399

Table 3. Features of the 57 proteins identified *in silico* that share homology with other membrane proteins

aa	pI	Res/ TM	TM	AMPL annotation (family members)	Acc nb AtDB	Proteo- mics	Homology
434	10.1	54.2	8	Unknown function (1 mb)	At2g44520		Heme farnesyl transferase
318	10.0	63.6	5	Unknown function (3 mb)	At4g14690		Carotene binding protein
303	10.1	75.8	4	Beta -carotene hydroxylase family (2 mb)	At5g52570		Beta-carotene hydroxylase
310	9.4	77.5	4	Beta -carotene hydroxylase family (2 mb)	At4g25700		Beta -carotene hydroxylase
530	9.2	88.3	6	Squalene epoxidase-like family (6 mb)	At4g37760		Squalene epoxidase
386	10.4	64.3	6	Unknown function (1 mb)	At4g22330		Ceramidase (<i>A. thaliana</i>)
438	10.1	54.8	8	Putative CDP-DG synthetase family (3 mb)	At4g26770		Putative CDP-diacylglycerol synthetase
310	10.0	77.5	4	1-acylglycerol-3-P acyltransferase family (4 mb)	At3g57650		1-acylglycerol-3-phosphate acyltransferase-like
233	10.1	38.8	6	Phosphatidyl glycerol-P synthase family (2 mb)	At3g55030		Phosphatidyl glycerophosphate synthase-like
296	10.9	49.3	6	Phosphatidyl glycerol-P synthase family (2 mb)	At2g39290		CDP-diacylglycerol-glycerol-3-P 3-phosphatidyltransferase
417	9.3	34.8	12	putative UDO-GlcNAc:dolichol-P GlcNAc-1-P transferase family (2 mb)	At2g41490		UDO-GlcNAc:dolichol-P GlcNAc-1-P transferase
289	11.1	36.1	8	Unknown function (4 mb)	At4g36830		NS1/SUR4 (yeast): fatty acid biosynthesis
281	10.5	40.1	7	Unknown function (4 mb)	At1g75000		Fatty acid biosynthesis
317	9.6	79.2	4	Unknown function (1 mb)	At1g78140		C5-O methyltransferase
189	10.0	47.2	4	Unknown function (1 mb)	At1g67740		Putative photosystem II core complex protein
219	10.3	54.8	4	Unknown function (1 mb)	At4g12800		Probable photosystem I chain IX precursor
551	9.9	55.1	10	Unknown function (1 mb)	At2g18710		Preprotein translocase SECY (thylakoids)
556	8.9	55.6	10	Unknown function (1 mb)	At2g31530		Preprotein translocase SECY (thylakoids)
347	10.0	43.4	8	Unknown function (1 mb)	At5g17520		Root cap 1 (RCP1)
264	10.1	66	4	Senescence-associated protein family (7 mb)	At5g23030		Senescence-associated protein 5-like protein
339	9.0	37.7	9	Wax synthase-like protein family (12 mb)	At5g55320		Wax synthase-like protein
390	9.8	97.5	4	Putative alpha/beta hydrolase family (3 mb)	At3g29770		Alpha/beta hydroxylase
326	9.6	46.6	7	Unknown function (1 mb)	At1g48270		Putative G-protein-coupled receptor (Cyclic AMP- receptor)
247	8.9	41.2	6	Unknown function (3 mb)	At5g47120		Bax inhibitor-like protein
341	9.4	34.1	10	Unknown function (4 mb)	At1g43650		Nodulin-like protein (MtN21)
359	9.4	35.9	10	Nodulin-like protein family (43 mb)	At5g64700		Nodulin-like protein (MtN21)
285	9.1	40.7	7	Mtn3-like protein family (16 mb)	At5g23660		MtN3-like (nodulin)
294	9.8	42	7	Mtn3-like protein family (16 mb)	At5g50800		MtN3-like (nodulin)
277	8.9	34.6	8	Mtn3-like protein family (16 mb)	At3g14770		MtN3-like (nodulin)
484	8.8	60.5	8	Unknown function (2 mb)	At4g39030		DNA damage inducible protein <i>Synechocystis</i>
239	9.3	59.8	4	Unknown function (4 mb)	At3g57280		Low homology inner envelope membrane protein
457	10.7	57.1	8	Unknown function (1 mb)	At5g56090		Cytochrome C oxidase assembly factor
462	9.2	77	6	Unknown function (3 mb)	At2g34020		Low homology Ca ⁺ binding protein
372	10.2	53.1	7	Unknown function (2 mb)	At2g16800		Urease accessory protein
243	10.1	48.6	5	Unknown function (1 mb)	At2g42770	HP25	PMP22 peroxisomal membrane protein
190	11.3	47.5	4	Unknown function (1 mb)	At4g04470		PMP22; cf. P25
288	10.9	72.0	4	Unknown function (1 mb)	At5g19750		PMP22; cf. P25
247	10.9	49.4	5	Unknown function (2 mb)	At3g51140	HP28	<i>Synechocystis</i> protein
348	10.1	58	6	Unknown function (1 mb)	At4g28210		<i>Synechocystis</i> protein
296	10.8	74	4	Unknown function (1 mb)	At2g15290		<i>Synechocystis</i> protein
367	9.8	73.4	5	Unknown function (1 mb)	At1g10830		<i>Synechocystis</i> protein
243	10.7	48.6	5	Unknown function (2 mb)	At5g62720	IEP18	<i>Synechocystis</i> protein
304	9.7	43.4	7	Unknown function (2 mb)	At5g04490		<i>Synechocystis</i> protein
344	8.9	57.3	6	Unknown function (1 mb)	At1g22850		<i>Synechocystis</i> protein
313	9.6	52.2	6	Unknown function (1 mb)	At4g18270		<i>Synechocystis</i> protein
333	10.4	55.5	6	Unknown function (1 mb)	At1g78620	HP34	<i>Synechocystis</i> protein
381	11.0	54.4	7	Unknown function (1 mb)	At3g21580		<i>Synechocystis</i> protein
267	10.4	66.8	4	Unknown function (1 mb)	At3g26710		<i>Synechocystis</i> protein
598	8.9	39.9	15	Unknown function (1 mb)	At3g45040		<i>Synechocystis</i> protein
272	9.8	68	4	Unknown function (1 mb)	At3g61870	HP29b	<i>Synechocystis</i> protein
213	9.9	53.2	4	Unknown function (1 mb)	At5g36120		<i>Synechocystis</i> protein
275	9.6	55	5	Unknown function (1 mb)	At1g26180		<i>Synechocystis</i> protein
307	9.0	51.2	6	Unknown function (2 mb)	At5g58560		<i>Synechocystis</i> protein
280	8.9	40	7	Unknown function (1 mb)	At1g28140		<i>Synechocystis</i> protein
287	10.1	71.8	4	Unknown function (1 mb)	At2g20920		<i>Synechocystis</i> protein
262	9.1	65.5	4	Unknown function (2 mb)	At5g13720	HP29c	-
512	10.1	39.4	13	Unknown function (1 mb)	At1g32080	HP45	-

Note that (i) several proteins appear to be associated with pigment or lipid metabolisms, (ii) only four of the selected proteins correspond to known or putative thylakoid membrane components, and (iii) many proteins of unknown function share homology with *Synechocystis* proteins. Other hypothetical proteins are not shown.